App. No.: 10/009873   Docket No.: SHW-009US
Inventor: Anand RANGANATHAN
Title: DNA MANIPULATION METHODS AND APPLICATIONS
  FOR SYNTHETIC ENZYMES
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(SEQ ID NO.: 1) 5' AAATCTAGACCC3'   XbaI RECOGNITION SEQUENCE
3'T TTAGATCTGGG5'

Add GA 5' upstream of the XbaI site

(SEQ ID NO.: 2) 5' AGATCTAGACCC3'
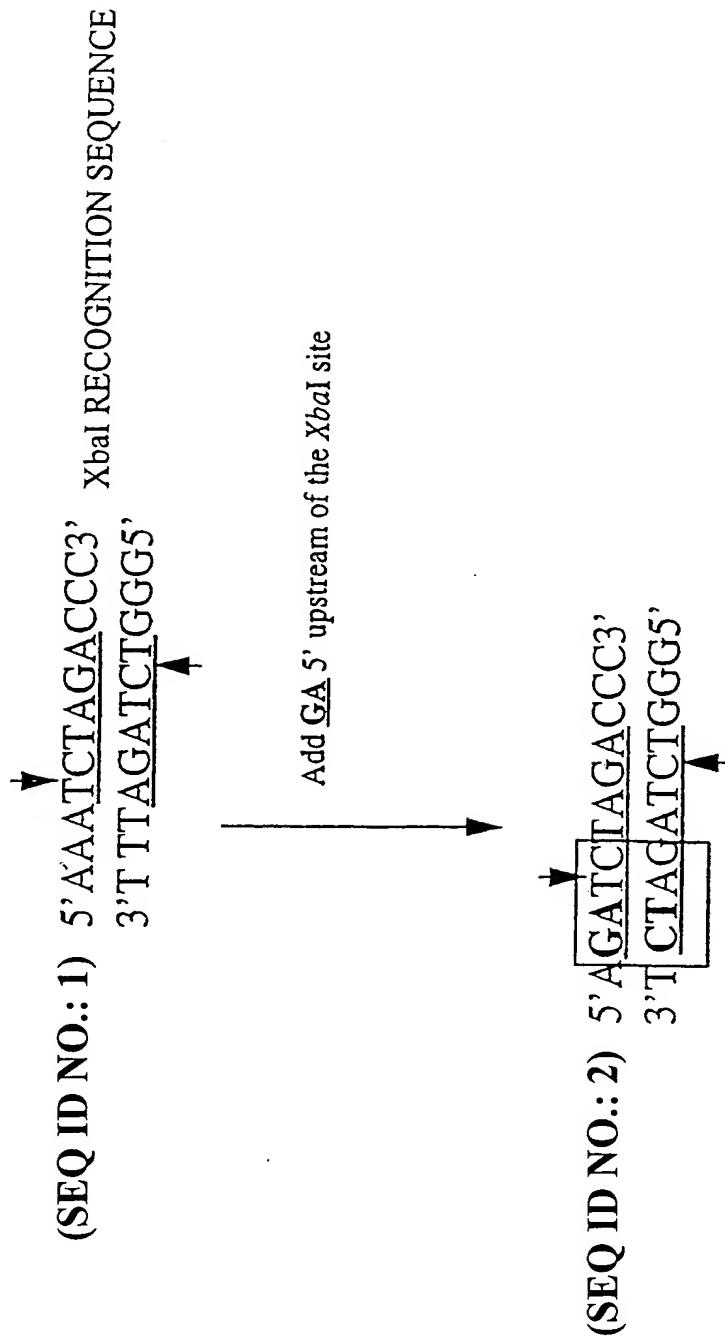3'T CTAGATCTGGG5'

FIG.6.

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S.l.    1 MAGTDREKALDAALAQIERQFGKGAVRMGDRTNEPIEVIPTGSTALDVA 50
          ||||||||||||||||||||||||||||||||· |||||||||||||||
S.a.    1 MAGTDREKALDAALAQIERQFGKGAVRMGDRSKEPIEVIPTGSTALDVA 50

       51 LGVGGIPRGRVVEVYGPESSGKTTLTLHAVANAQKAGGQVAFVDAEHALD 100
          |||||:|||||:|||||||||||||||||||||||||||||||||||||
       51 LGVGGLPRGRVIEVYGPESSGKTTLTLHAVANAQKAGGQVAFVDAEHALD 100

      101 PEYAKKLGVDIDNLILSQPDNGEQALEIVDMLVRSGALDLIVIDSVAALV 150
          ||||·||||||||||||||||||||||||||||||||||||||||||||
      101 PEYAQKLGVDIDNLILSQPDNGEQALEIVDMLVRSGALDLIVIDSVAALV 150

      151 PRAEIEGEMGDSHVGLQARLMSQALRKITSALNQSKTTAIFINQLREKIG 200
          |||||||||||||||||||||||||||||||||||||||||||||||||
      151 PRAEIEGEMGDSHVGLQARLMSQALRKITSALNQSKTTAIFINQLREKIG 200

      201 VMFGSPETTTGGRALKFYASVRLDIRRIETLKDGTDAVGNRTRVKVVKNK 250
          |||||||||||||||||||||||||||||||||||||||||||||||||
      201 VMFGSPETTTGGRALKFYASVRLDIRRIETLKDGTDAVGNRTRVKVVKNK 250

      251 VAPPFKQAEFDILYGQGISREGGLIDMGVENGFVRKAGAWYTYEGDQLGQ 300
          |||||||||||||||||||||||||||||·|||||||||||||||||||
      251 VAPPFKQAEFDILYGQGISREGGLIDMGVEHGFVRKAGAWYTYEGDQLGQ 300

      301 GKENARNFLKDNPDLANEIEKKIKQKLGVGVHPEE.SATEPGADAASAAP 349
          |||||||||||||||||||||||||||:||||||| ||| ·||| | |||·
      301 GKENARNFLKDNPDLANEIEKKIKEKLGVGVRPEEPTATESGPDAAT... 347

      350 ADAAPAVPAPTTAKATKSKAAAAKS 374 (SEQ ID NO.: 3)
          |:·|||||||| ||| ||·|||||||
      348 AESAPAVPAPATAKVTKAKAAAAKS 372 (SEQ ID NO.: 4)
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FIG.13.

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S.l.   1 ATGGCAGGAACCGACCGCGAGAAGGCCCTGGACGCCGCGCTCGCACAGAT 50
          ||||||||||||||||||||||||||||| || ||||||||| |||||||||||
S.a.   1 ATGGCAGGAACCGACCGCGAGAAGGCTCTTGACGCCGCACTCGCACAGAT 50

       51 TGAACGGCAATTCGGCAAGGGCGCGGTCATGCGCATGGGTGACCGGACCA 100
          ||||||||| |||||||||||||||||||||||||||||||||| |||||| | |
       51 TGAACGGCAGTTCGGCAAGGGCGCGGTCATGCGCATGGGCGACCGGTCGA 100

      101 ACGAGCCCATCGAGGTCATCCCGACCGGGTCTACCGCGCTCGACGTGGCC 150
          | ||||||||||||||||||||||||||||||||| |||||||||||||||
      101 AGGAGCCCATCGAGGTCATCCCGACCGGGTCGACCGCGCTCGACGTGGCC 150

      151 CTCGGCGTCGGAGGCATCCCGCGTGGCCGTGTCGTGGAGGTCTACGGCCC 200
          |||||||||| ||| | |||||| ||||| ||| | ||||||||||| ||
      151 CTCGGCGTCGGCGGCCTGCCGCGCGGCCGCGTCATCGAGGTCTACGGTCC 200

      201 CGAGTCCTCGGGCAAGACGACCCTGACCCTGCACGCGGTGGCGAACGCGC 250
          ||||||||| || |||||||||||||||||||||| |||||||||||||||
      201 GGAGTCCTCCGGTAAGACGACCCTGACCCTGCACGCCGTGGCGAACGCGC 250

      251 AGAAGGCCGGCGGCCAGGTCGCGTTCGTGGACGCCGAGCACGCCCTCGAC 300
          |||||||||||||||||||| ||||||||||||||| ||||||||||||||
      251 AGAAGGCCGGCGGCCAGGTGGCGTTCGTGGACGCGGAGCACGCCCTCGAC 300

      301 CCCGAGTACGCGAAGAAGCTCGGTGTCGACATCGACAACCTGATCCTGTC 350
          |||||||||| ||||||||||| |||||||||||||||||||||||||||
      301 CCCGAGTACGCCCAGAAGCTCGGCGTCGACATCGACAACCTGATCCTGTC 350

      351 CCAGCCGGACAACGGTGAGCAGGCCCTGGAGATCGTGGACATGCTGGTCC 400
          |||||||||||||||||||||||||||||||||||||||||||||||||||
      351 CCAGCCGGACAACGGTGAGCAGGCCCTGGAGATCGTGGACATGCTGGTCC 400

      401 GCTCCGGCGCCCTCGACCTCATCGTCATCGACTCCGTCGCCGCGCTCGTC 450
          |||||||||||||||||||||||||||||||||||||||||||||||||||
      401 GCTCCGGCGCCCTCGACCTCATCGTCATCGACTCCGTCGCCGCGCTCGTC 450

      451 CCGCGCGCGGAGATCGAGGGCGAGATGGGCGACAGCCACGTCGGTCTGCA 500
          |||||||||||||||||||||||||||||| |||||||||||||||||| ||
      451 CCGCGCGCGGAGATCGAGGGCGAGATGGGTGACAGCCACGTCGGTCTCCA 500

      501 GGCCCGGCTGATGAGCCAGGCCCTGCGGAAGATCACCAGCGCGCTCAACC 550 (SEQ ID NO.: 5)
          ||||||||||||||||||||| || ||||||||||||||||||||||||||
      501 GGCCCGGCTGATGAGCCAGGCGCTCCGGAAGATCACCAGCGCGCTCAACC 550 (SEQ ID NO.: 6)

FIG.14.A.

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S.l.   551 AGTCCAAGACCACCGCGATCTTCATCAACCAGCTCCGCGAGAAGATCGGC 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||
S.a.   551 AGTCCAAGACCACCGCGATCTTCATCAACCAGCTCCGCGAGAAGATCGGC 600

       601 GTGATGTTCGGCTCCCCGGAGACCACGACCGGTGGCCGGGCACTGAAGTT 650
           ||  ||||||||||||||||||||||||||||||||||||||| ||  |||||
       601 GTCATGTTCGGCTCCCCGGAGACCACGACCGGTGGCCGGGCGCTCAAGTT 650

       651 CTACGCCTCGGTGCGACTCGACATCCGGCGTATCGAGACGCTGAAGGACG 700
           |||||||||||||||||||||||||| || |||||||||||| |||||||
       651 CTACGCCTCGGTGCGACTCGACATCCGACGCATCGAGACGCTCAAGGACG 700

       701 GCACCGACGCGGTCGGCAACCGCACCCGCGTCAAGGTGGTCAAGAACAAG 750
           ||||||||||||||||||||||||| ||||||||| |||||||||||||
       701 GCACCGACGCGGTCGGCAACCGCACGCGCGTCAAGGTCGTCAAGAACAAG 750

       751 GTCGCGCCGCCCTTCAAGCAGGCCGAGTTCGACATCCTCTACGGCCAGGG 800
           ||||||||||||||||||||||||||||||||||||||||||||||||||
       751 GTCGCGCCGCCCTTCAAGCAGGCCGAGTTCGACATCCTCTACGGCCAGGG 800

       801 CATCAGCCGCGAGGGCGGTCTGATCGACATGGGCGTGGAGAACGGCTTCG 850
           ||||||||||||||||| |||||||||||||||||||||||| |||||||
       801 CATCAGCCGCGAGGGCGGCCTGATCGACATGGGCGTGGAGCACGGCTTCG 850

       851 TCCGCAAGGCCGGCGCCTGGTACACGTACGAGGGCGACCAGCTCGGTCAG 900
           |||||||||||||||||||||||||||||||||||||||||||||| |||
       851 TCCGCAAGGCCGGCGCCTGGTACACGTACGAGGGCGACCAGCTCGGCCAG 900

       901 GGCAAGGAGAACGCGCGCAACTTCCTGAAGGACAACCCCGACCTGGCCAA 950
           |||||||||||||||||||||||||||||||||||||||||||| |||||
       901 GGCAAGGAGAACGCGCGCAACTTCCTGAAGGACAACCCCGACCTCGCCAA 950

       951 CGAGATCGAGAAGAAGATCAAGCAGAAGCTGGGCGTCGGCGTGCACCCCG 1000
           ||||||||||||||||||||||| ||||||||||||||||| || |   |||
       951 CGAGATCGAGAAGAAGATCAAGGAGAAGCTGGGCGTCGGAGTCCGTCCCG 1000

      1001 AGGA...GTCGGCCACCGAGCCCGGCGCGGACGCCGCCTCCGCCGCCCCG 1047
           ||||   | ||||||||||| ||||   |||            |||||| ||
      1001 AGGAGCCGACGGCCACCGAGTCCGGACCGGA.........CGCCGCGACG 1041

      1048 GCCGACGCCGCACCGGCGGTGCCCGCACCCACGACCGCCAAGGCCACCAA 1097
           |||||   |||||||||||||||||||||| ||| |||||||||||| |||||
      1042 GCCGAATCCGCACCGGCGGTGCCCGCGCCCGCGACCGCCAAGGTCACCAA 1091

      1098 GTCCAAGGCCGCGGCAGCCAAGAGCTGA 1125 (SEQ ID NO.: 5)
           | |||||||||||||||||||||||||||
      1092 GGCCAAGGCCGCGGCAGCCAAGAGCTGA 1119 (SEQ ID NO.: 6)
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FIG.14.B.